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Research Article

Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oriza sativa* L.)

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ABSTRACT

This study was conducted during summer 2015 at Regional Agriculture Research Station, Dipayal, Doti, Nepal to estimate the genotypic and phenotypic variability, heritability, genetic advance and correlation on grain yield and yield associated traits using 26 advance genotypes of lowland irrigated rice. Analysis of variance revealed the existence of significant difference for days to flowering, maturity, plant height, panicle length, thousand grain weight and grain yield. High heritability was estimated for days to flowering (0.88), maturity (0.79), thousand grain weight (0.48) and plant height (0.43) suggesting these traits are under high genetic control. High phenotypic variation was observed for grain yield (24.87%), number of grains/panicle (22.45%), number of panicles/m^2 (20.95%) and straw yield (20.75%) while grain yield had medium (12.02%) and remaining traits showed low genotypic coefficient of variation (<10%). High phenotypic coefficient of variation estimated as compared to genotypic coefficient of variation showed environmental influence on the expression of traits. Grain yield (11.98) and days to flowering (10.32) showed medium and remaining traits sowed low genotypic advance as percent of mean. High to low heritability with moderate to low genotypic advance as percent of mean suggested these traits were governed by non additive gene thus direct selection is not beneficial. Further improvements on yield potentiality and yield traits on these genotypes are suggested by creating variation and selection. Panicle length (r = 0.230), days to flowering (r = 0.247), effective tillers (r = 0.488) and straw yield (r = 0.846) manifested significant positive association with grain yield indicating that yield can be increased if selection applied in favor of those yield components.

Keywords: Rice, variability, heritability, genetic advance, correlation

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INTRODUCTION

Rice (*Oryza sativa* L.) is the one of the staple food for one third of the world population after maize and wheat. It is widely grown in tropical and subtropical regions (Ezuka and Kaku, 2000). Rice found in Asia, America and Europe belongs to *Oryza sativa* and varieties grown in West Africa belong to *Oryza glaberrima*. The *sativa* rice species are commonly divided in to three subspecies namely; *Indica*, *Japonica* and *Javanica*.

Nepal is rich in rice diversity and more than 1, 700 rice landraces are reported in Nepal growing from 60 to 3, 050 m altitude (Mallick, 1981). Rice ranks the first crop in terms of area, production and livelihood of the people. At national level, rice is cultivated in an area of nearly 1.36 million hectares with an annual production of 4.29 million tones and productivity of 3154kg ha^{-1} (MOAD, 2017). It is grown in three agro-ecological regions (terai and inner terai, mid hills and high hills under irrigated, rain-fed lowland and upland production environment (MOAD, 2015). Terai is the main rice cultivation area produced 70 percent of the total rice, while the hills and mountain contribute 26 percent and 4 percent respectively. The normal rice (main season) occupies about 92 percent rice cultivated area. Being principal staple food of Nepalese, rice supplies about 40% of the food calorie intake and contributes 20% to the agricultural gross domestic product (AGDP) and 7% to national GDP (MOAD, 2015). Recognizing the importance of rice in different aspects of Nepalese life, Government of Nepal started to celebrate Asar 15 (last week of June) as National Rice Day since 2004 with the aim to increase rice production by creating awareness about the importance of rice. However, despite its importance in food security and national economy, still more than 35 percent rice is grown under rainfed condition. Therefore, rice production statistics in Nepal largely depends on amount, distribution and onset of rainfall. Lack of adaptable drought tolerance varieties, diseases pest infestation, fertilizers management are major limiting factors on rice production. The area under rice in Nepal has decreased about 10% in last 10 years (2005-2015) because of utilization of rice land for industrialization and urbanization while productivity has just increased by 15% during the time. Hence, increasing rice yields on existing land remains the primary strategy for increasing production, to meet the future demand for food, for increasing population. Globally additional 176 million tons rice is required by 2035, which can be fulfilled by increase yield potential from 10 to 12.3 tons per hectare (Khush, 2013). Phenotypic variability is the differences between individuals in a population due to genetic composition and growing environment (Sumanth *et al.,* 2017). Planning and execution of any breeding program for improvement on quantitative traits depends on magnitude of genetic variability. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder (Adhikari *et al.,* 2018). Variability, genetic diversity, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait. Heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a trait in a population and shows the component of a character transmitted to future generations. Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under

selection than heritability alone. In addition relationship between yield and yield attributing traits are prime important for direct and indirect selection of traits to which contributes to yield (Aditya & Bhartiya, 2013). Therefore, the study was under taken to know information on variability, heritability, genetic advance and traits correlation in promising rice genotypes to develop suitable genotype for rainfed, drought prone areas of Nepal.

MATERIALS AND METHOD

Experimental Location, Experimental Design, and Planting Materials

The experiment was conducted at Regional Agricultural Research Station, Dipayal, Doti. Geographically, it is situated at 80° 55' east longitude and 29° 15' north latitude and the altitude of this station is 510 masl (RARS, 2015). In general, the climate is sub tropical, Pre- monsoon period is dry and very hot. Monsoon starts very late in July and it is very erratic. Generally, annual rainfall does not exceed 1000 ml. High solar radiation and wide variation in day and night temperature is the climatic features of the area. Experimental field soil was shallow in depth and porous, sandy loam, slightly acidic with pH 5.5-6.0, low in nitrogen and organic matter i.e. 1-2% and 0.6 % respectively. Because of light texture soil and low organic matter content, the water holding capacity of the soil is very low. Twenty six rice genotypes (Table 1) received from National Rice Research Program, Hardinath was experimented on randomized complete block design in 3 replications during rainy season of 2015.

Table 1. List of Rice genotypes used for the study

Seed Source	SN	Genotypes	SN	Genotypes	SN	Genotypes
NRRP, Hardinath	1	IR83754-B-B-40-2	10	IR75417-R-R-R-26	19	IR84859-B-86-3-1
	2	IR87761-28-1-1-3	11	IR70210-39-CPA-7-1	20	IR88869-2-1-1-4
	3	IR83387-B-B-117-4	12	IR80408-B-43-3	21	IR88869-2-1-1-4
	4	IR83380-B-B-124-2	13	IR82870-48	22	IR88965-19-3-1-2
	5	08 FAN-6	14	IR79906-192-2-3	23	IR966-1-1-2-3
	6	BP1356-IG-KN-4	15	IR87754-42-2-2	24	IR87875-207-B-B-B
	7	IR09F4-36	16	IR83750-B-B-13-1-1	25	Hardinath-1
	8	IR82635-B-B-58-1	17	IR88964-11-2-2-2	26	Radha-4
	9	IR82635-B-B-25-4	18	IR88966-45-2-1-3		

Cultural Practices

Seed was shown on flat bed @ 50 kg ha^{-1} on 23rd June and 25 days old seedlings were transplanted with 2-3 seedlings per hills on puddle field. In addition to FYM @ 6 t ha^{-1}, chemical fertilizer @ 40: 60: 40 N P_2O_5 K_2O kg ha^{-1} was applied during field preparation and top dressing was done by @ N 40 kg ha^{-1} after 40 days of transplanting. Spacing used was 25 cm between rows and 15 cm between hills in a row. Individual plot size was 6 m^2.

Data Collection

Morphological data were collected at appropriate growth stage by adopting the standard evaluation system indicated by IRRI (2002). Ten plants from middle row of each plot were randomly selected and plant height, panicle length, fertile grains per panicle were taken. Effective tillers, number of panicles were taken from 1m^2 area from the middle of the plot. Days to flowering and maturity were taken on plot basis. Grain yield and straw yield were taken from individual plots by excluding 3 border rows on both sides. Thousand grain weight was taken at 14% moisture content. Grain yield was adjusted to 14% moisture and straw yield was recorded after one week of sun drying after threshing.

Statistical analysis

Analysis of variance and correlation among traits were done by using Genstat 18th edition at 0.05 level of significance. Likewise significance of correlation coefficient was done as proposed by Kothari (2004). The phenotypic and genotypic variances were computed according to Falconer (1981). Broad sense heritability was calculated using formula suggested by Allard (1960). The estimates of genetic advance were obtained and categorized as high, medium and low as suggested by Johnson *et al.* (1955). Coefficient of genotypic and phenotypic variation were categorized as proposed by Sivasubramanian and Madhavamenon (1973).

RESULTS AND DISCUSSION

Agronomic performance

The analysis of variance for 10 quantitative characters showed highly significant differences among the evaluated genotypes for days to flowering, days to maturity, plant height, thousand grain weight and panicle length while significant difference was observed for grain yield kg ha^{-1} (Table 2). However, differences were not significant for straw yield kg ha^{-1}, effective tillers/m^2, number of panicles/m^2 and number of filled grains/panicle. This indicated inherent genetic variation among evaluated genotypes for grain yield, days to flowering, days to maturity, panicle length and plant height. Thus there is possibility of genetic improvement through selection and hybridization for significant traits on tested genotypes. This result is very similar with Poudel *et.al.* (2014) and Gyawali *et al.* (2018). Significant genetic variability among rice genotypes for yield and major yield attributing traits were also reported by Poudel *et al.* (2014), Gyawali *et al.* (2018), Bekele *et al.* (2013), Rashid *et al.* (2017), Summanth *et al.* (2017), Abebe *et al.* (2017) and Bandhi *et al.* (2018).

Table 2 Analysis of Variance (ANOVA) for yield and contributing traits

SN	Trait	Rep	Treatment	Error	F cal	LSD(0.05)	CV%	P value
1	DF	6.16	66.61	2.86	23.29	2.77	2.0	<0.001
2	DM	2.70	83.15	6.86	12.12	4.29	2.2	<0.001
3	ET/m^2	868.10	427.9	302.8	1.41		15.2	0.147
4	PH	355.65	175.14	53.76	3.25	12.02	6.9	<0.001
5	P/m2	96027	4199	2499	1.68		18.9	0.059
6	PL	66.39	6.5	2.23	2.91	2.45	5.5	<0.001
7	G/P	222.40	933	622	1.50		20.8	0.111
8	TGW	1.76	3.51	0.93	10.8	2.56	10.8	<0.001
9	SY	76.01	9.59	5.99	1.60	4.01	19.0	0.078
10	GY	10.85	3.16	1.65	1.91	2112.2	21.8	0.026

DF= Days to 50% flowering, DM= Days to 85% maturity, ET/m^2 = Number of effective tillers m^2, PH= Plant height (cm), P/m^2= Number of panicles/m^2, PL= Panicle length (cm), G/P= Number of filled grains/panicle, TGW= Thousand grain weight (g), SY= Straw yield (t ha^{-1}), GY = Grain Yield (t ha^{-1})

Mean value for 10 quantitative characters were presented in Table 3. Rice genotypes showed considerable phenotypic variation on observed characters. None of the test genotypes found early in heading and maturity than standard check variety Hardinath-1. Earliness is a desired trait particularly for rainfed rice-wheat cropping system where wheat is grown on residual moisture Delay on rice harvesting will delay wheat sowing which adversely affect wheat germination and growth because of moisture stress on delay sown condition. Thus, Hardinath-1 may be a parent in rice breeding program focused on rice-wheat system. Straw yield is another selection criteria for rice variety as it is valuable for livestock feed. Genotypes IR09F4-36 produced significantly higher straw yield check variety Hardinath-1. Genotypes IR09F4-36, IR88965-19-3-1-2 were produced higher yield than check variety. Therefore on the basis of grain yield, maturity, thousand grain weight and straw yield genotypes IR09F4-36, IR88965-19-3-1-2 and IR79906-192-2-3 were found superior and recommended for rainfed rice wheat system.

Table 3. Agronomic performance of rice genotypes

SN	Genotypes	DF	DM	ET	PH	P/m^2	PL	G/P	TGW	GY	SY
1	IR83754-B-B-40-2	84	117	121	117	221	27	141	14.9	4.2 ^{abc}	10.3
2	IR87761-28-1-1-3	87	122	99	108	270	31	121	13.8	6.0 ^{abcde}	12.8
3	IR83387-B-B-117-4	88	121	100	111	263	27	141	14.7	5.7 ^{abcde}	13.0
4	IR83380-B-B-124-2	85	117	100	107	262	25	92	13.3	5.7 ^{abcde}	13.3
5	08 FAN-6	91	126	93	114	277	28	106	13.2	4.4 ^{ab}	9.6
6	BP1356-IG-KN-4	84	115	125	91	309	27	77	13.9	6.3 ^{abcde}	12.2
7	IR09F4-36	90	125	128	99	281	28	119	14.4	7.8 ^{e}	15.5
8	IR82635-B-B-58-1	84	118	110	108	245	28	132	14.2	4.6 ^{abcd}	10.0
9	IR82635-B-B-25-4	82	114	100	113	245	26	138	15.5	5.6 ^{abcde}	14.3
10	IR75417-R-R-R-26	83	118	126	119	271	25	129	15.4	4.2^{ac}	11.0
11	IR70210-39-CPA-7-1	86	123	98	115	296	26	118	13.9	5.3c^{abcde}	12.0
12	IR80408-B-43-3	86	121	110	116	208	27	119	16.0	6.5c^{abcde}	15.4
13	IR82870-48	84	114	97	103	311	29	117	15.0	6.0c^{abcde}	13.5
14	IR79906-192-2-3	91	119	132	110	278	28	106	13.7	7.0c^{cde}	15.3
15	IR87754-42-2-2	87	114	97	118	216	28	131	15.9	6.0c^{abcde}	14.6
16	IR83750-B-B-13-1-1	89	122	98	107	240	28	125	13.7	5.8 ^{abcde}	12.2
17	IR88964-11-2-2-2	89	121	120	99	256	25	109	13.9	6.4 ^{abcde}	13.2
18	IR88966-45-2-1-3	94	128	125	103	278	28	118	15.3	7.1 ^{cde}	14.1
19	IR84859-B-86-3-1	83	116	110	101	211	28	487	13.8	4.6 ^{abcde}	11.0
20	IR88869-2-1-1-4	88	120	155	108	283	26	162	14.0	7.4 ^{cde}	14.6
21	IR88869-2-1-1-4	88	123	130	101	243	28	135	14.6	6.9 ^{bcde}	13.5
22	IR88965-19-3-1-2	84	117	135	99	237	27	115	15.7	7.4 ^{de}	15.1
23	IR966-1-1-2-3	94	128	127	98	323	29	119	13.9	6.6 ^{cde}	14.4
24	IR87875-207-B-B-B	89	124	119	101	359	26	91	15.4	6.0 ^{abcde}	13.4
25	HARDINATH-1	70	103	132	96	209	26	130	14.5	5.0 ^{abcd}	10.3
26	RADHA-4	86	118	97	98	279	24	116	14.1	5.1 ^{abcd}	11.3
	Mean	86	120	115	107	264	27	135	14.5	5.9	13.0

Means followed by a superscripted common letter with in a column are not significantly different from each other at P ≤ 0.05. DF= Days to 50% flowering, DM= Days to 85% maturity, ET/m^2 = Number of effective tillers m^2, PH= Plant height (cm), P/m^2= Number of panicles/m^2, PL= Panicle length (cm), G/P= Number of filled grains/panicle, TGW= Thousand grain weight (g), SY= Straw yield (t ha^{-1}), GY = Grain Yield (t ha^{-1})

Genetic variability, Heritability and Genetic advance

Mean, range along with the variability estimates such as the phenotypic coefficient of variation (PCV), the genotypic coefficient of variation (GCV), broad sense heritability, and genetic advance as percent of means are presented in Table 4. Phenotypic coefficient of variance was found higher than genotypic coefficient of variance for all studied traits indicate the environmental influence on the expression of these traits. Similar results were presented by (Malimar *et al.,* 2015; Rashid *et al.,* 2017; Gyawali *et al.,* 2018). The extent of the influence of

growing environment on observed traits is explained by the magnitude of the differences between GCV and PCV. Large difference between PCV and GCV indicate high environmental influence on the expression of particular traits. In the present study, phenotypic coefficient of variation in general were higher than genotypic coefficient of variation for all the traits indicating high environmental effect on the expression of these traits except days to heading (PCV 5.68, GCV 5.34) and maturity (PCV 4.76 and GCV 4.22) which were less affected by environment for expression. Thus, selection based on phenotypic performance for days to flowering and maturity would be effective to bring about considerable genetic improvement. Higher phenotypic variation (PCV) was observed for grain yield (24.87%), number of grains/panicles (22.45%), Number of panicles/m^2 (20.95%) and Straw yield (20.75%) where as number of effective tillers/m^2 (16.18%) showed medium phenotypic coefficient of variation and among the studied traits days to flowering, days to maturity, panicle length, thousand grain weight and plant height showed low phenotypic coefficient of variation (Table 4). Grain yield kg ha^{-1} had medium (12.02%) and remaining traits showed low genotypic coefficient of variation (<10%).

Table 4 Mean, range, phenotypic (Vp) and genotypic variance (Vg), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), heritability (broad sense), genetic advance (GA) and genetic advance as percent of mean (GAM) for observed traits

SN	Trait	Mean	Range	Vg	Vp	Hbs	GCV	PCV	GA	GAM
1	DF	86.40	70-94.3	21.25	24.11	0.88	5.34	5.68	8.92	10.32
2	DM	119.50	144.3-128	25.43	32.29	0.79	4.22	4.76	9.22	7.71
3	ET	114.70	92.7-134.7	41.70	344.50	0.12	5.63	16.18	4.63	4.04
4	PH	106.20	91.3-118.3	40.46	94.22	0.43	5.99	9.14	8.59	8.09
5	P/m2	264.30	208.7-359.3	566.67	3065.67	0.18	9.01	20.95	21.08	7.98
6	PL	27.22	24.3-29.3	1.42	3.65	0.39	4.38	7.02	1.53	5.64
7	G/P	120.00	77.3-140.7	103.67	725.67	0.14	8.48	22.45	7.93	6.61
8	TGW	14.50	13.2-16.0	0.86	1.79	0.48	6.4	9.23	1.32	9.13
9	SY	12.92	9.62-15.54	1.20	7.19	0.17	8.48	20.75	0.92	7.14
10	GY	5.90	4.19-7.83	0.50	2.15	0.23	12.02	24.87	0.71	11.98

DF= Days to 50% flowering, DM= Days to 85% maturity, ET/m^2 = Number of effective tillers m^2, PH= Plant height (cm), P/m^2= Number of panicles/m^2, PL= Panicle length (cm), G/P= Number of filled grains/panicle, TGW= Thousand grain weight (g), SY= Straw yield (t ha^{-1}), GY = Grain Yield (t ha^{-1})

Very similar findings were reported by Gyawali *et al.* (2018). High PCV on grain yield was also reported by (Ajmera *et al.,* 2017; Abebe *et al.,* 2017) which is in agreement with this present study. The greater difference between GCV and PCV were observed in number of grains per panicle, grain yield, straw yield, number of panicles/m^2, number of effective tillers/m^2 and thousand grain weight indicating that these traits were more influenced by growing environment can be improved by providing optimum growing environments Likewise small difference between GCV and PCV were observed on panicle length, plant height, days to flowering and days to maturity indicated that there was very little environmental influence on these traits and cannot be improved by providing favorable environment. In general, high coefficient of variability shows scope of selection in favour of traits of interest and low coefficient of variability indicates the need for creation of variability and selection.

Among the studied traits broad sense heritability ranged from 0.12 (effective tillers/m^2 to 0.88 days to flowering. Heritability is grouped as low (<0.2), moderate (0.2-0.4) and high (>0.4). Days to flowering (0.88), days to maturity (0.79), thousand grain weight (0.48) and plant height (0.43) were observed highly heritable traits. Panicle length (0.39) and grain yield (0.23) showed moderately heritable traits whereas number of panicles/m^2 (0.18), straw yield (0.17), grains/panicle (0.14) and effective tillers/m^2 (0.12) showed low heritability. Similar reports were reported by Gyawali *et al.* (2018), Bandi *et al.* (2018), Aditya and Bhartiya (2013) for days to flowering, maturity, thousand grain weight and similarly by Gyawali *et al.* (2018) for grain yield. High to medium level heritability for grain yield was reported by Gyawali *et al.* (2018), Bandhi *et al.* (2018), Abebe *et al.* (2017) may be due to the influence of the environment on the yield as it is polygenic trait. Low heritability estimates might be due to the variation of environmental component involved for those traits and vice versa. High heritability estimated traits indicated a high response to selection for particular traits.

Estimated heritability itself alone is not very much useful because it includes the effect of both additive and non additive gene. The genetic advance is therefore a useful indicator to achieve expected result on the trait of interest of a population after selection. Genetic advance in percentage of mean give more precise result in comparison to only genetic advance. Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20% and high (≥20%). In the present study moderate genetic advance as percent of mean was estimated for grain yield kg ha^{-1} (11.98%) and other traits showed low genetic advances (<10%). This indicates observed characters among tested genotypes governed by non-additive gene action and thus heterosis breeding, family selection and progeny testing methods is used for improvement on such traits. Low genetic advance as percent of mean was also estimated by Abebe *et al.* (2018) for days to maturity, effective tillers, grains/panicle, number of panicles and thousand grain weight which is quite similar to the present findings. In addition similar reporting was made by Mallimar *et al.* (2015) for maturity, panicle length and thousand grain weight and moderate genetic advance for grain yield and low genetic advance for thousand grain weight, panicle length and effective tillers on rice were also reported by Singh *et al.* (2011).

Correlation coefficient is a measure of the degree association and relationship between two variables. It is important in plant breeding as it can be used for indirect selection. The study of correlation between different characters may help the plant breeder to know how the improvement of one character will bring simultaneous changes in other characters. Degree of correlation is categorized as weak (0-0.3), moderate (0.3-0.7) and strong (0.7-1.0). Phenotypic correlation between grain yield and yield attributing traits of twenty six rice genotypes is presented in the Table 5. Rice yield showed strong positive correlation to straw yield (r = 0.846**), moderate positive with effective tillers (r = 0.488**) and weak positive with days to flowering (r = 0.247*), panicle length (r = 0.23*), thousand grain weight (r = 0.101), grains/panicle (r = 0.055) and panicles/m^2 (r = 0.017). Therefore selection based on these traits would be effective to increase yield. These results are closely similar with (Aditya & Bhitiya, 2013) except for plant height and Gywali *et al.* (2018) (except for straw yield). Positive correlation of panicle length, thousand grain weight, straw yield on grain yield was also reported

by Kumar *et al.* (2018). Similarly Bhatt *et al.* (2015) also reported positive correlation of effective tillers, panicle length and grains per panicles on the rice yield which is supportive to the present findings.

Flowering days showed strong positive correlation with days to maturity (r = 0.796**) indicated that selection on early flowering types can use to select early maturing population. Aditya and Bhitiya (2013), Ogunbayo *et al.* (2014) and Kumar *et al.* (2018) also reported significant positive correlation between days to flowering and maturity. Similarly flowering days has weak positive association with panicles per square meter (r = 0.260*), panicle length (r = 0.147), straw yield (r = 0.190*) and grain yield (r = 0.247*) explained these traits can be improve by selecting late flowering types. Weak negative association with days to flowering were found on effective tillers per square meter (r = -0.059), plant height (r = -0.028), grains per panicle (r = -0.07) and thousand grain weight (r = -0.045) which was also supported by Kumar *et al.* (2018).

Table 5 Phenotypic correlation coefficients between 10 quantitative characters of rice

	DF	DM	ET/m^2	PH	P/m^2	PL	G/P	TGW	SY
DF									
DM	0.796**								
ET/m^2	-0.059	-0.027							
PH	-0.028	0.047	-0.061						
P/m^2	0.260*	0.206	0.018	-0.349**					
PL	0.147	0.091	0.131	0.137	-0.306**				
G/P	-0.070	-0.031	-0.021	0.281*	-0.278*	0.125			
TGW	-0.045	-0.080	0.388**	-0.008	0.098	-0.097	0.116		
SY	0.190*	0.114	0.486**	0.189	-0.052	0.196	0.064	0.084	
GY	0.247*	0.193	0.488**	-0.060	0.017	0.230*	0.055	0.101	0.846**

***Significant at 0.01 probability level, *Significant at 0.05 probability level*
DF= Days to 50% flowering, DM= Days to 85% maturity, ET/m^2 = Number of effective tillers m^2, PH= Plant height (cm), P/m^2= Number of panicles/m^2, PL= Panicle length (cm), G/P= Number of filled grains/panicle, TGW= Thousand grain weight (g), SY= Straw yield (t ha^{-1}), GY = Grain Yield (t ha^{-1})

Plant height showed weak negative correlation with grain yield (r = -0.060), thousand grain weight (r = -0.008), days to flowering (r = -0.028) and effective tillers per square meter (r = -0.061) indicated that these traits can be steadily improve by selecting dwarf plant type. In addition, significant negative moderate correlation (r = -0.349**) between plant height and number of panicles per square meter indicate effectiveness on panicles density improvement by selecting dwarf plant types. On the other side, plant height showed weak positive correlation with panicle length (r = 0.137), grains per panicle (r = 0.281*), straw yield (r = 0.189) and days to maturity (r = 0.047). Similar findings were reported by Gywali *et al.* (2018) which support the present findings. In addition, Kumar *et al.* (2015) reported similar correlations for days to flowering, effective tillers, panicle length, straw yield with respect to plant height whereas contradictory correlation were reported for days to maturity, 1000 grain weight and grain yield with respect to height. Correlation between days to maturity and other traits were observed nominal. Weak positive association were observed for number of harvested panicles per square meter, panicle length, straw yield, plant height and grain yield however effective tillers per

square meter, grains per panicle and thousand grain weight showed weak negative relationship which is supported by (Kumar *et al.,* 2015) except for panicle length.

Effective tillers was found to show moderate positive correlation with thousand grain weight (r =0.338**), straw yield (r = 0.486**) and grain yield (r = 0.488**) ; weak positive with panicle length (r = 0.131) and panicles per square meter conformed the contribution of tillering capacity towards increase grain boldness, straw yield, panicle length and grain yield of rice. These results were in conformity with Gywali *et al.* (2018). Panicle length had shown positive correlation with grains per panicle (r = 0.125), straw yield (r = 0.196), grain yield (r = 0.230*) and negative relation with thousand grain weight (r = -0.097). Similarly weak positive correlations were observed for grains per panicles and thousand grain weight towards straw and grain yield. Positive correlation between panicle length and grain yield were also reported by (Aditya & Bhitiya, 2013; Ogunbayo *et al.,* 2014; Bhatt *et al.,* 2015; Gywali *et al.,* 2018; Kumar *et al.,* 2018). Overall correlation results between yield and yield attributing traits indicated that selection directed towards favoring higher panicle number per plant, effective tillers per square meter, test weight and straw weight and medium plant height with moderate grain number and optimum days to flowering would be effective to achieve higher grain yield on rice.

CONCLUSION

This study generally indicated that there was genetic variability among the genotypes studied mostly inheritance by non additive gene action, hence direct selection is not fruitful on these populations. Thus hybridization, mutation breeding then selection and progeny testing methods is recommended for improvement on traits of interest. Selection applied in favour of days to flowering, effective tillers, panicle length and straw yield will chance yield potential of rice genotypes as these traits manifested significant positive association with grain yield. On the basis of mean performance, high grain yield, maturity, thousand grain weight were exhibited by the genotypes IR09F4-36, IR88965-19-3-1-2 and IR79906-192-2-3 which were found suitable genotypes for cultivation in rainfed rice wheat system.

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Authors contribution

B. N. Adhikari	Designed and performed experiment, analysed data and wrote the paper
B. P. Joshi	Performed experiment, data recorded
J. Shrestha	Wrote and edit manuscript
N. R. Bhatta	Helped in experiment and data recording

Conflict of interest

The authors declare that there is no conflicts of interest regarding publication of this manuscript.

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